

Supplementary Box 1. Issues in inferring absolute dates

A goal of many population genomic analyses is to infer effective population sizes and dates in calendar time. However, from population genomic data alone, such inferences are impossible. This is because population genetic data depends on *population scaled* parameters, such as $\theta = 4N\mu$ which is a product of the effective population size (N) and the mutation rate (μ) and *population scaled* times, typically $t = \tau/2N$ where τ is the time in generations. To tease apart these compound parameters, an estimate of the mutation rate is often used.

Until the past few years, the best estimates of the human mutation rate came from phylogenetic calibrations. These estimates arise by using fossil data to time-calibrate genetic divergence times between species. Based primarily on fossil calibrations of the human-macaque divergence, and an assumption of a 25-year generation time, a commonly assumed mutation rate in humans was $2.0\text{--}2.5 \times 10^{-8}$ per site per generation¹. Despite causing some controversy about the status of certain fossils said to be putative human ancestors, this estimate enjoyed widespread use.

However, advances in technology now enable “direct” calculation of the mutation rate via sequencing of parent-offspring trios^{2–5}. Several studies in both humans and chimpanzees have suggested that the current mutation rate may be close to half that inferred from phylogenetic data. While some researchers¹ argue that recent estimates of the mutation rate are more similar to each other than one might expect by chance, it is generally acknowledged that the human mutation rate is substantially slower than previously thought.

The linear scaling of estimates of absolute dates and effective sizes with mutation rate has caused substantial confusion regarding the timing of important events in human history. Similarly, this uncertainty has caused renewed controversy about the status of putative human ancestors⁶ and the association of population sizes and divergence events with paleoclimate data.